SEQUENCE LISTING

<110> Hinuma, Shujii

<110> Kawamata, Yuji

<110> Fujii, Ryo

<110> Matsumoto, Hirokazu

<120> Prolactin Secretion Modulator

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<150> PCT/JP98/02765

<151> 1998-06-22

<150> JP 9-165437

<151> 1997-06-23

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            20                  25                  30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
        35                  40                  45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro
    50                  55                  60
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
65                  70                  75                  80
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
                85                  90                  95
Gln Glu
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<210> 2

<211> 294

<212> DNA

<213> Bovine

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GCTGCCAGCA GAGCCCACCA GCACTCCATG GAGATCCGCA CCCCCGACAT CAACCCTGCC 120
TGGTACGCRG GCCGTGGGAT CCGGCCCGTG GGCCGCTTCG GCCGGCGAAG AGCTGCCCYG 180
GGGGACGGAC CCAGGCCTGG CCCCCGGCGT GTGCCGGCCT GCTTCCGCCT GGAAGGCGGY 240
GCTGAGCCCT CCCGAGCCCT CCCGGGGCGG CTGACGGCCC AGCTGGTCCA GGAA 294

<210> 3

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<212> PRT

<213> Bovine

<400> 3

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly
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<210> 4

<211> 19

<212> PRT

<213> Bovine

<400> 4

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg
19

<210> 5

<211> 31

<212> PRT

<213> Bovine

<400> 5

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1 5 10 15
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

<210> 6

<211> 32

<212> PRT

<213> Bovine

<400> 6

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 7

<211> 33

<212> PRT

<213> Bovine

<400> 7

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30
Arg
33

<210> 8

<211> 20

<212> PRT

<213> Bovine

<400> 8

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe
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<210> 9

<211> 21

<212> PRT

<213> Bovine

<400> 9

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly
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<210> 10

<211> 22

<212> PRT

<213> Bovine

<400> 10

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly Arg
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<210> 11

<211> 87

<212> DNA

<213> Bovine

<400> 11

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GCRGGCCGTG GGATCCGGCC CGTGGGC 87

<210> 12

<211> 57

<212> DNA

<213> Bovine

<400> 12

ACCCCCGACA TCAACCCTGC CTGGTACGCR GGCCGTGGGA TCCGGCCCGT GGGCCGC 57

<210> 13

<211> 93

<212> DNA

<213> Bovine

<400> 13

AGCAGAGCCC ACCAGCACTC CATGGAGATC CGCACCCCCG ACATCAACCC TGCCTGGTAC 60
GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTC 93

<210> 14

<211> 96

<212> DNA

<213> Bovine

<400> 14

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GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGC 96

<210> 15

<211> 99

<212> DNA

<213> Bovine

<400> 15

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GCRGGCCGTG GGATCCGGCC CGTGGGCCGC TTCGGCCGG 99

<210> 16

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<212> DNA

<213> Bovine

<400> 16

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<210> 17

<211> 63

<212> DNA

<213> Bovine

<400> 17

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GGC 63

<210> 18

<211> 66

<212> DNA

<213> Bovine

<400> 18

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<210> 19

<211> 91

<212> PRT

<213> Human

<400> 19

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 1               5                  10                  15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
            20                  25                  30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
        35                  40                  45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
    50                  55                  60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65                  70                  75                  80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile
                85                  90
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<210> 20

<211> 59

<212> PRT

<213> Human

<400> 20

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Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu
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Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
            20                  25                  30
Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
        35                  40                  45
Thr Phe Cys Leu Leu Val Val Val Val Val Val
    50                  55
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<210> 21

<211> 370

<212> PRT

<213> Human

<400> 21

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Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
 1               5                  10                  15
Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
            20                  25                  30
Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
        35                  40                  45
Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
    50                  55                  60
Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
65                  70                  75                  80
Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
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                85                  90                  95
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
            100                 105                 110
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
        115                 120                 125
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
    130                 135                 140
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
145                 150                 155                 160
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
                165                 170                 175
Ala Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
            180                 185                 190
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
        195                 200                 205
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
    210                 215                 220
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
225                 230                 235                 240
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
                245                 250                 255
Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
            260                 265                 270
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala
        275                 280                 285
Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp
    290                 295                 300
Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys
305                 310                 315                 320
His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala
                325                 330                 335
Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala
            340                 345                 350
Trp Pro Arg Lys Ile Ala Pro His Gly Gln Asn Met Thr Val Ser Val
        355                 360                 365
Val Ile
    370
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<210> 22

<211> 206

<212> PRT

<213> Murine

<400> 22

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Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu Tyr Asn Val Thr Asn
 1               5                  10                  15
Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
            20                  25                  30
Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
        35                  40                  45
Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr
    50                  55                  60
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65                  70                  75                  80
Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
                85                  90                  95
Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
            100                 105                 110
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
        115                 120                 125
Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
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    130                 135                 140
Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145                 150                 155                 160
Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
                165                 170                 175
Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
            180                 185                 190
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
        195                 200                 205
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<210> 23

<211> 126

<212> PRT

<213> Murine

<400> 23

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Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
 1               5                  10                  15
Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
            20                  25                  30
Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
        35                  40                  45
Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile
    50                  55                  60
Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala
65                  70                  75                  80
Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
                85                  90                  95
Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
            100                 105                 110
Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
        115                 120                 125
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<210> 24

<211> 273

<212> DNA

<213> Human

<400> 24

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AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCGGCTG GGTGTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGGTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATC                               273
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<210> 25

<211> 177

<212> DNA

<213> Human

<400> 25

GGCCTGCTGC TGGTCACCTA CCTGCTCCCT CTGCTGGTCA TCCTCCTGTC TTACGTCCGG 60
GTGTCAGTGA AGCTCCGCAA CCGCGTGGTG CCGGGCTGCG TGACCCAGAG CCAGGCCGAC 120
TGGGACCGCG CTCGGCGCCG GCGCACCTTC TGCTTGCTGG TGGTGGTCGT GGTGGTG 177

<210> 26

<211> 1110

<212> DNA

<213> Human

<400> 26

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GCGGTCACAA CTCCCGCCAA CCAGAGCGCA GAGGCCTCGG CGGGCAACGG GTCGGTGGCT 120
GGCGCGGACG CTCCAGCCGT CACGCCCTTC CAGAGCCTGC AGCTGGTGCA TCAGCTGAAG 180
GGGCTGATCG TGCTGCTCTA CAGCGTCGTG GTGGTCGTGG GGCTGGTGGG CAACTGCCTG 240
CTGGTGCTGG TGATCGCGCG GGTGCGCCGG CTGCACAACG TGACGAACTT CCTCATCGGC 300
AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 360
GCCTTCGAGC CACGCGGCTG GGTGTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG 420
CAGCCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 480
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 540
CTGGCCATCT GGGCGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 600
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 660
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 720
ATCCTCCTGT CTTACGTCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCTGC 780
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 840
GTGGTGGTCG TGGTGGTGTT CGCCGTCTGC TGGCTGCCGC TGCACGTCTT CAACCTGCTG 900
CGGGACCTCG ACCCCCACGC CATCGACCCT TACGCCTTTG GGCTGGTGCA GCTGCTCTGC 960
CACTGGCTCG CCATGAGTTC GGCCTGCTAC AACCCCTTCA TCTACGCCTG GCTGCACGAC 1020
AGCTTCCGCG AGGAGCTGCG CAAACTGTTG GTCGCTTGGC CCCGCAAGAT AGCCCCCCAT 1080
GGCCAGAATA TGACCGTCAG CGTGGTCATC 1110

<210> 27

<211> 618

<212> DNA

<213> Murine

<400> 27

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AACCTGGCCT TGTCCGACGT GCTCATGTGC ACCGCCTGCG TGCCGCTCAC GCTGGCCTAT 120
GCCTTCGAGC CACGCGGCTG GGTGTTCGGC GGCGGCCTGT GCCACCTGGT CTTCTTCCTG 180
CAGGCGGTCA CCGTCTATGT GTCGGTGTTC ACGCTCACCA CCATCGCAGT GGACCGCTAC 240
GTCGTGCTGG TGCACCCGCT GAGGCGGCGC ATCTCGCTGC GCCTCAGCGC CTACGCTGTG 300
CTGGCCATCT GGGTGCTGTC CGCGGTGCTG GCGCTGCCCG CCGCCGTGCA CACCTATCAC 360
GTGGAGCTCA AGCCGCACGA CGTGCGCCTC TGCGAGGAGT TCTGGGGCTC CCAGGAGCGC 420
CAGCGCCAGC TCTACGCCTG GGGGCTGCTG CTGGTCACCT ACCTGCTCCC TCTGCTGGTC 480
ATCCTCCTGT CTTACGCCCG GGTGTCAGTG AAGCTCCGCA ACCGCGTGGT GCCGGGCCGC 540
GTGACCCAGA GCCAGGCCGA CTGGGACCGC GCTCGGCGCC GGCGCACCTT CTGCTTGCTG 600
GTGGTGGTCG TGGTGGTG 618

<210> 28

<211> 378

<212> DNA

<213> Murine

<400> 28

GTGGTTCTGG TGCACCCGCT ACGTCGGCGC ATTTCACTGA GGCTCAGCGC CTACGCGGTG 60
CTGGGCATCT GGGCTCTATC TGCAGTGCTG GCGCTGCCGG CCGCGGTGCA CACCTACCAT 120
GTGGAGCTCA AGCCCCACGA CGTGAGCCTC TGCGAGGAGT TCTGGGGCTC GCAGGAGCGC 180
CAACGCCAGA TCTACGCCTG GGGGCTGCTT CTGGGCACCT ATTTGCTCCC CCTGCTGGCC 240
ATCCTCCTGT CTTACGTACG GGTGTCAGTG AAGCTGAGGA ACCGCGTGGT GCCTGGCAGC 300
GTGACCCAGA GTCAAGCTGA CTGGGACCGA GCGCGTCGCC GCCGCACTTT CTGTCTGCTG 360
GTGGTGGTGG TGGTAGTG 378

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<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 29

CGTGGSCMTS STGGGCAACN YCCTG 25

<210> 30

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 30

GTNGWRRGGC ANCCAGCAGA KGGCAAA 27

<210> 31

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 31

CTGTGYGYSA TYGCNNTKGA YMGSTAC 27

<210> 32

<211> 29

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 32

AKGWAGWAGG GCAGCCAGCA GANSRYGAA 29

<210> 33

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 33

CTGACTTATT TTCTGGGCTG CCGC 24

<210> 34

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 34

AACACCGACA CATAGACGGT GACC 24

<210> 35

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 35

GCICAYCARC AYTGYATGGA 20

<210> 36

<211> 26

<212> DNA

<213> Unknown

<220>

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CCIACGGGIC KDATGCCICK GCCIGC 26

<210> 37

<211> 26

<212> DNA

<213> Unknown

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ACGGGCCKDA TGCCICKGCC IGCRTA 26

<210> 38

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 38

CCGGCGTACC AGGCAGGGTT 20

<210> 39

<211> 28

<212> DNA

<213> Unknown

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<210> 40

<211> 27

<212> DNA

<213> Unknown

<220>

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<400> 40

CTGCCAGCAG AGCCCACCAG CACTCCA 27

<210> 41

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 41

GTGGGGGCCT GGCTCCTCTG CCTGCTG 27

<210> 42

<211> 32

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 42

GTGTCGACGA ATGAAGGCGG TGGGGGCCTG GC 32

<210> 43

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 43

AGGCTCCCGC TGTTATTCCT GGAC 24

<210> 44

<211> 98

<212> PRT

<213> Bovine

<400> 44

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Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
 1               5                  10                  15
Ala Leu Gln Gly Ala Ala Ser Arg Ala His Gln His Ser Met Glu Ile
            20                  25                  30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
        35                  40                  45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro
    50                  55                  60
Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
65                  70                  75                  80
Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
                85                  90                  95
Gln Glu
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<210> 45

<211> 83

<212> PRT

<213> Rat

<400> 45

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Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Leu Ser Leu Val
 1               5                  10                  15
Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg
            20                  25                  30
Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
        35                  40                  45
Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly
    50                  55                  60
Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser
65                  70                  75                  80
Gln Arg Gly
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<210> 46

<211> 249

<212> DNA

<213> Rat

<400> 46

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TCCAGCCGAG CCCACCAGCA CTCCATGGAG ACAAGAACCC CTGATATCAA TCCTGCCTGG 120
TACACGGGCC GCGGGATCAG GCCTGTGGGC CGCTTCGGCA GGAGAAGGGC AACCCCGAGG 180
GATGTCACTG GACTTGGCCA ACTCAGCTGC CTCCCACTGG ATGGACGCAC CAAGTTCTCT 240
CAGCGTGGA 249

<210> 47

<211> 31

<212> PRT

<213> Rat

<400> 47

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

<210> 48

<211> 32

<212> PRT

<213> Rat

<400> 48

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 49

<211> 33

<212> PRT

<213> Rat

<400> 49

Ser Arg Ala His Gln His Ser Met Glu Thr Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

20 25 30

Arg

<210> 50

<211> 20

<212> PRT

<213> Rat

<400> 50

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe
20

<210> 51

<211> 21

<212> PRT

<213> Rat

<400> 51

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly
20

<210> 52

<211> 22

<212> PRT

<213> Rat

<400> 52

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly Arg
20

<210> 53

<211> 93

<212> DNA

<213> Rat

<400> 53

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC 60

ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTC 93

<210> 54

<211> 96

<212> DNA

<213> Rat

<400> 54

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC 60
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGC 96

<210> 55

<211> 99

<212> DNA

<213> Rat

<400> 55

AGCCGAGCCC ACCAGCACTC CATGGAGACA AGAACCCCTG ATATCAATCC TGCCTGGTAC 60
ACGGGCCGCG GGATCAGGCC TGTGGGCCGC TTCGGCAGG 99

<210> 56

<211> 60

<212> DNA

<213> Rat

<400> 56

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

<210> 57

<211> 63

<212> DNA

<213> Rat

<400> 57

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGC 63

<210> 58

<211> 66

<212> DNA

<213> Rat

<400> 58

ACCCCTGATA TCAATCCTGC CTGGTACACG GGCCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGCAGG 66

<210> 59

<211> 87

<212> PRT

<213> Human

<400> 59

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu
1 5 10 15
Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile
20 25 30
Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg
35 40 45
Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro
50 55 60
Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly
65 70 75 80
Ala Met Ser Ser Gln Asp Gly
85

<210> 60

<211> 261

<212> DNA

<213> Human

<400> 60

ATGAAGGTGC TGAGGGCCTG GCTCCTGTGC CTGCTGATGC TGGGCCTGGC CCTGCGGGGA 60
GCTGCAAGTC GTACCCATCG GCACTCCATG GAGATCCGCA CCCCTGACAT CAATCCTGCC 120
TGGTACGCCA GTCGCGGGAT CAGGCCTGTG GGCCGCTTCG GTCGGAGGAG GGCAACCCTG 180
GGGGACGTCC CCAAGCCTGG CCTGCGACCC CGGCTGACCT GCTTCCCCCT GGAAGGCGGT 240
GCTATGTCGT CCCAGGATGG C 261

<210> 61

<211> 31

<212> PRT

<213> Human

<400> 61

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe

20 25 30

<210> 62

<211> 32

<212> PRT

<213> Human

<400> 62

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 63

<211> 33

<212> PRT

<213> Human

<400> 63

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15
Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30
Arg

<210> 64

<211> 20

<212> PRT

<213> Human

<400> 64

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe
20

<210> 65

<211> 21

<212> PRT

<213> Human

<400> 65

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro

1 5 10 15
Val Gly Arg Phe Gly
20

<210> 66

<211> 22

<212> PRT

<213> Human

<400> 66

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Gly Arg
20

<210> 67

<211> 93

<212> DNA

<213> Human

<400> 67

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GCCAGTCGCG GGATCAGGCC TGTGGGCCGC TTC 93

<210> 68

<211> 96

<212> DNA

<213> Human

<400> 68

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<210> 69

<211> 99

<212> DNA

<213> Human

<400> 69

AGTCGTACCC ATCGGCACTC CATGGAGATC CGCACCCCTG ACATCAATCC TGCCTGGTAC 60
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<210> 70

<211> 60

<212> DNA

<213> Human

<400> 70

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60

<210> 71

<211> 63

<212> DNA

<213> Human

<400> 71

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GGT 63

<210> 72

<211> 66

<212> DNA

<213> Human

<400> 72

ACCCCTGACA TCAATCCTGC CTGGTACGCC AGTCGCGGGA TCAGGCCTGT GGGCCGCTTC 60
GGTCGG 66

<210> 73

<211> 21

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 10th position is Ala or Thr.
Xaa of the 11th position is Gly or Ser.
Xaa of the 21st position is H, Gly or GlyArg.

<400> 73

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro
1 5 10 15
Val Gly Arg Phe Xaa
20

<210> 74

<211> 11

<212> PRT

<213> Unknown

<220>

<223> Unsure. Xaa of the 3rd position is Ala or Thr.
Xaa of th- 5th position is Gln or Arg.
Xaa of the 10th position is Ile or Thr.

<400> 74

Ser Arg Xaa His Xaa His Ser Met Glu Xaa Arg
1 5 10

<210> 75

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 75

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<210> 76

<211> 24

<212> DNA

<213> Unknown

<220>

<223> Unsure

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TACCAGGCAG GATTGATACA GGGG 24

<210> 77

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 77

GGCATCATCC AGGAAGACGG AGCAT 25

<210> 78

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

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AGCAGAGGAG AGGGAGGGTA GAGGA 25

<210> 79

<211> 22

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 79

ACGTGGCTTC TGTGCTTGCT GC 22

<210> 80

<211> 25

<212> DNA

<213> Unknown

<220>

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<400> 80

GCCTGATCCC GCGGCCCGTG TACCA 25

<210> 81

<211> 26

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 81

TTGCCCTTCT CCTGCCGAAG CGGCCC 26

<210> 82

<211> 27

<212> DNA

<213> Unknown

<220>

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GGCGGGGGCT GCAAGTCGTA CCCATCG 27

<210> 83

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CGGCACTCCA TGGAGATCCG CACCCCT 27

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<211> 27

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<213> Unknown

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CAGGCAGGAT TGATGTCAGG GGTGCGG 27

<210> 85

<211> 27

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CATGGAGTGC CGATGGGTAC GACTTGC 27

<210> 86

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 86

GGCCTCCTCG GAGGAGCCAA GGGATGA 27

<210> 87

<211> 27

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 87

GGGAAAGGAG CCCGAAGGAG AGGAGAG 27

<210> 88

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 88

CCTGCTGGCC ATTCTCCTGT CTTAC 25

<210> 89

<211> 25

<212> DNA

<213> Unknown

<220>

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<400> 89

GGGTCCAGGT CCCGCAGAAG GTTGA 25

<210> 90

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 90

GAAGACGGAG CATGGCCCTG AAGAC 25

<210> 91

<211> 25

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 91

GGCAGCTGAG TTGGCCAAGT CCAGT 25

<210> 92

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 92

Ser Arg Ala His Gln His Ser Met Glu Ile Arg Thr Pro Asp Cys
1 5 10 15

<210> 93

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 93

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
1 5 10 15

<210> 94

<211> 15

<212> PRT

<213> Unknown

<220>

<223> Unsure

<400> 94

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly
1 5 10 15

<210> 95

<211> 30

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 95

AGATTGGCAT CATCCAGGAA GACGGAGCAT 30

<210> 96

<211> 31

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 96

GCTGACTCGA CAGCACTGTC TTCTCGAGCT G 31

<210> 97

<211> 21

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 97

AACCCCTTCA TCTATGCGTG G 21

<210> 98

<211> 20

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 98

ATATTCTGGC CATGAGGCAC 20

<210> 99

<211> 28

<212> DNA

<213> Unknown

<220>

<223> Unsure

<400> 99

TTCCGAGAGG AGCTACGCAA GATGCTTC 28